

PCT09

RAW SEQUENCE LISTING

DATE: 07/27/2001

PATENT APPLICATION: US/09/673,222

TIME: 20:05:25

Input Set : A:\04765-1.txt

Output Set: N:\CRF3\07272001\I673222.raw

ENTERED

3 <110> APPLICANT: Vale, Ronald
 4 Hartman, James
 6 <120> TITLE OF INVENTION: Assays for the Detection of Microtubule Depolymerization
 Inhibitors

8 <130> FILE REFERENCE: UCSD-04765
 10 <140> CURRENT APPLICATION NUMBER: 09/673,222
 11 <141> CURRENT FILING DATE: 2000-10-13
 13 <150> PRIOR APPLICATION NUMBER: PCT/US99/08086
 14 <151> PRIOR FILING DATE: 1999-04-13
 16 <150> PRIOR APPLICATION NUMBER: 60/081,734
 17 <151> PRIOR FILING DATE: 1998-04-14
 19 <160> NUMBER OF SEQ ID NOS: 16
 21 <170> SOFTWARE: PatentIn version 3.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 517
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Strongylocentrotus purpuratus
 28 <220> FEATURE:
 29 <221> NAME/KEY: misc_feature
 30 <223> OTHER INFORMATION: katanin p60 subunit
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 36 1 5 10 15
 38 Ala Leu Leu Gly Asn Tyr Glu Thr Ser Leu Val Tyr Tyr Gln Gly Val
 39 20 25 30
 41 Leu Gln Gln Ile Gln Lys Leu Leu Thr Ser Val His Glu Pro Gln Arg
 42 35 40 45
 44 Lys His Gln Trp Gln Thr Ile Arg Gln Glu Leu Ser Gln Glu Tyr Glu
 45 50 55 60
 47 His Val Lys Asn Ile Thr Lys Thr Leu Asn Gly Phe Lys Ser Glu Pro
 48 65 70 75 80
 50 Ala Ala Pro Glu Pro Ala Pro Asn His Gly Arg Ala Ala Pro Phe Ser
 51 85 90 95
 53 His His Gln His Ala Ala Lys Pro Ala Ala Glu Pro Ala Arg Asp
 54 100 105 110
 56 Pro Asp Val Trp Pro Pro Pro Thr Pro Val Asp His Arg Pro Ser Pro
 57 115 120 125
 59 Pro Tyr Gln Arg Ala Ala Arg Lys Asp Pro Pro Arg Ser Glu Pro
 60 130 135 140
 62 Ser Lys Pro Ala Asn Arg Ala Pro Gly Asn Asp Arg Gly Gly Arg Gly
 63 145 150 155 160
 65 Pro Ser Asp Arg Arg Gly Asp Ala Arg Ser Gly Gly Gly Gly Arg Gly
 66 165 170 175
 68 Gly Ala Arg Gly Ser Asp Lys Asp Lys Asn Arg Gly Gly Lys Ser Asp
 69 180 185 190
 71 Lys Asp Lys Lys Ala Pro Ser Gly Glu Glu Gly Asp Glu Lys Lys Phe
 72 195 200 205
 74 Asp Pro Ala Gly Tyr Asp Lys Asp Leu Val Glu Asn Leu Glu Arg Asp

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75      210      215      220
77 Ile Val Gln Arg Asn Pro Asn Val His Trp Ala Asp Ile Ala Gly Leu
78 225      230      235      240
80 Thr Glu Ala Lys Arg Leu Leu Glu Glu Ala Val Val Leu Pro Leu Trp
81      245      250      255
83 Met Pro Asp Tyr Phe Lys Gly Ile Arg Arg Pro Trp Lys Gly Val Leu
84      260      265      270
86 Met Val Gly Pro Pro Gly Thr Gly Lys Thr Met Leu Ala Lys Ala Val
87      275      280      285
89 Ala Thr Glu Cys Gly Thr Thr Phe Phe Asn Val Ser Ser Ala Ser Leu
90      290      295      300
92 Thr Ser Lys Tyr His Gly Glu Ser Glu Lys Leu Val Arg Leu Leu Phe
93 305      310      315      320
95 Glu Met Ala Arg Phe Tyr Ala Pro Ser Thr Ile Phe Ile Asp Glu Ile
96      325      330      335
98 Asp Ser Ile Cys Ser Lys Arg Gly Thr Gly Ser Glu His Glu Ala Ser
99      340      345      350
101 Arg Arg Val Lys Ser Glu Leu Leu Ile Gln Met Asp Gly Val Ser Gly
102      355      360      365
104 Pro Ser Ala Gly Glu Glu Ser Ser Lys Met Val Met Val Leu Ala Ala
105      370      375      380
107 Thr Asn Phe Pro Trp Asp Ile Asp Glu Ala Leu Arg Arg Arg Leu Glu
108 385      390      395      400
110 Lys Arg Ile Tyr Ile Pro Leu Pro Glu Ile Asp Gly Arg Glu Gln Leu
111      405      410      415
113 Leu Arg Ile Asn Leu Lys Glu Val Pro Leu Ala Asp Asp Ile Asp Leu
114      420      425      430
116 Lys Ser Ile Ala Glu Lys Met Asp Gly Tyr Ser Gly Ala Asp Ile Thr
117      435      440      445
119 Asn Val Cys Arg Asp Ala Ser Met Met Ala Met Arg Arg Arg Ile Gln
120      450      455      460
122 Gly Leu Arg Pro Glu Glu Ile Arg His Ile Pro Lys Glu Glu Leu Asn
123 465      470      475      480
125 Gln Pro Ser Thr Pro Ala Asp Phe Leu Leu Ala Leu Gln Lys Val Ser
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132      515
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135 <211> LENGTH: 690
136 <212> TYPE: PRT
137 <213> ORGANISM: Strongylocentrotus purpuratus
139 <220> FEATURE:
140 <221> NAME/KEY: misc_feature
141 <223> OTHER INFORMATION: katanin p80 subunit
144 <400> SEQUENCE: 2
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149 Ser Asn Val Asn Cys Leu Ala Leu Gly Pro Met Ser Gly Arg Val Met
150          20          25          30
152 Val Thr Gly Gly Glu Asp Lys Lys Val Asn Leu Trp Ala Val Gly Lys
153          35          40          45
155 Gln Asn Cys Ile Ile Ser Leu Ser Gly His Thr Ser Pro Val Asp Ser
156          50          55          60
158 Val Lys Phe Asn Ser Ser Glu Glu Leu Val Val Ala Gly Ser Gln Ser
159 65          70          75          80
161 Gly Thr Met Lys Ile Tyr Asp Leu Glu Pro Ala Lys Ile Val Arg Thr
162          85          90          95
164 Leu Thr Gly His Arg Asn Ser Ile Arg Cys Met Asp Phe His Pro Phe
165          100         105         110
167 Gly Glu Phe Val Ala Ser Gly Ser Thr Asp Thr Asn Val Lys Leu Trp
168          115         120         125
170 Asp Val Arg Arg Lys Gly Cys Ile Tyr Thr Tyr Lys Gly His Ser Asp
171          130         135         140
173 Gln Val Asn Met Ile Lys Phe Ser Pro Asp Gly Lys Trp Leu Val Thr
174 145         150         155         160
176 Ala Ser Glu Asp Thr Thr Ile Lys Leu Trp Asp Leu Thr Met Gly Lys
177          165         170         175
179 Leu Phe Gln Glu Phe Lys Asn His Thr Gly Gly Val Thr Gly Ile Glu
180          180         185         190
182 Phe His Pro Asn Glu Phe Leu Leu Ala Ser Gly Ser Ser Asp Arg Thr
183          195         200         205
185 Val Gln Phe Trp Asp Leu Glu Thr Phe Gln Leu Val Ser Ser Thr Ser
186          210         215         220
188 Pro Gly Ala Ser Ala Val Arg Ser Ile Ser Phe His Pro Asp Gly Ser
189 225         230         235         240
191 Tyr Leu Phe Cys Ser Ser Gln Asp Met Leu His Ala Phe Gly Trp Glu
192          245         250         255
194 Pro Ile Arg Cys Phe Asp Thr Phe Ser Val Phe Trp Gly Lys Val Ala
195          260         265         270
197 Asp Thr Val Ile Ala Ser Thr Gln Leu Ile Gly Ala Ser Phe Asn Ala
198          275         280         285
200 Thr Asn Val Ser Val Tyr Val Ala Asp Leu Ser Arg Met Ser Thr Thr
201          290         295         300
203 Gly Ile Ala Gln Glu Pro Gln Ser Gln Pro Ser Lys Thr Pro Ser Gly
204 305         310         315         320
206 Gly Ala Glu Glu Val Pro Ser Lys Pro Leu Thr Ala Ser Gly Arg Lys
207          325         330         335
209 Asn Phe Val Arg Glu Arg Pro His Thr Thr Ser Ser Lys Gln Arg Gln
210          340         345         350
212 Pro Asp Val Lys Ser Glu Pro Glu Arg Gln Ser Pro Thr Gln Asp Glu
213          355         360         365
215 Gly Val Lys Asp Asp Asp Ala Thr Asp Ile Lys Asp Pro Asp Ser Tyr
216          370         375         380
218 Ala Lys Ile Phe Ser Pro Lys Thr Arg Val Asp His Ser Pro Glu Arg
219 385         390         395         400
221 Asn Ala Gln Pro Phe Pro Ala Pro Leu Asp Val Pro Gly Ala Gln Glu

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222          405          410          415
224 Pro Glu Pro Phe Lys His Pro Pro Lys Pro Ala Ala Ala Ala Val
225          420          425          430
227 Ala Pro Val Ser Arg Ala Pro Ala Pro Ser Ala Ser Asp Trp Gln Pro
228          435          440          445
230 Ala Gln Ala Asn Pro Ala Pro Asn Arg Val Pro Ala Ala Thr Lys Pro
231          450          455          460
233 Val Pro Ala Gln Glu Val Ala Pro Ser Arg Lys Pro Asp Pro Ile Ser
234 465          470          475          480
236 Thr Ile Ile Pro Ser Asp Arg Asn Lys Pro Ala Asn Leu Asp Met Asp
237          485          490          495
239 Ala Phe Leu Pro Pro Ala His Ala Gln Ala Pro Arg Val Asn Ala
240          500          505          510
242 Pro Ala Ser Arg Lys Gln Ser Asp Ser Glu Arg Ile Glu Gly Leu Arg
243          515          520          525
245 Lys Gly His Asp Ser Met Cys Gln Val Leu Ser Ser Arg His Arg Asn
246          530          535          540
248 Leu Asp Val Val Arg Ala Ile Trp Thr Ala Gly Asp Ala Lys Thr Ser
249 545          550          555          560
251 Val Glu Ser Val Val Asn Met Lys Asp Gln Ala Ile Leu Val Asp Ile
252          565          570          575
254 Leu Asn Ile Met Leu Leu Lys Lys Ser Leu Trp Asn Leu Asp Met Cys
255          580          585          590
257 Val Val Val Leu Pro Arg Leu Lys Glu Leu Leu Ser Ser Lys Tyr Glu
258          595          600          605
260 Asn Tyr Val His Thr Ser Cys Ala Cys Leu Lys Leu Ile Leu Lys Asn
261          610          615          620
263 Phe Thr Ser Leu Phe Asn Gln Asn Ile Lys Cys Pro Pro Ser Gly Ile
264 625          630          635          640
266 Asp Ile Thr Arg Glu Arg Tyr Asn Lys Cys Ser Lys Cys Tyr Ser
267          645          650          655
269 Tyr Leu Ile Ala Thr Arg Gly Tyr Val Glu Glu Lys Gln His Val Ser
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272 Gly Lys Leu Gly Ser Ser Phe Arg Glu Leu His Leu Leu Leu Asp Gln
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276          690
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279 <211> LENGTH: 730
280 <212> TYPE: PRT
281 <213> ORGANISM: Xenopus laevis
283 <220> FEATURE:
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285 <223> OTHER INFORMATION: Xenopus kinesin central motor 1 (XKCM1)
288 <400> SEQUENCE: 3
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291 1          5          10          15
293 Ile Met Arg Ser Asn Gly Val Ile His Asn Ala Asn Ile Thr Ser Val
294          20          25          30

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```

296 Asn Met Asp Arg Ser Ser Val Asn Val Glu Trp Lys Glu Gly Glu Ala
297      35      40      45
299 Asn Lys Gly Lys Glu Ile Ser Phe Ala Asp Val Ile Ser Val Asn Pro
300      50      55      60
302 Glu Leu Leu Asp Ala Val Leu Ala Pro Thr Asn Val Lys Glu Asn Met
303 65      70      75      80
305 Pro Pro Gln Arg Asn Val Ser Ser Gln Asn His Lys Arg Lys Thr Ile
306      85      90      95
308 Ser Lys Ile Pro Ala Pro Lys Glu Val Ala Ala Lys Asn Ser Leu Leu
309      100     105     110
311 Ser Glu Ser Gly Ala Gln Ser Val Leu Arg Glu Arg Ser Thr Arg Met
312      115     120     125
314 Thr Ala Ile His Glu Thr Leu Pro Tyr Glu Asn Glu Met Glu Ala Glu
315      130     135     140
317 Ser Thr Pro Leu Pro Ile Gln Gln Asn Ser Val Gln Ala Arg Ser Arg
318 145      150     155     160
320 Ser Thr Lys Val Ser Ile Ala Glu Glu Pro Arg Leu Gln Thr Arg Ile
321      165     170     175
323 Ser Glu Ile Val Glu Glu Ser Leu Pro Ser Gly Arg Asn Asn Gln Gly
324      180     185     190
326 Arg Arg Lys Ser Asn Ile Val Lys Glu Met Glu Lys Met Lys Asn Lys
327      195     200     205
329 Arg Glu Glu Gln Arg Ala Gln Asn Tyr Glu Arg Arg Met Lys Arg Ala
330      210     215     220
332 Gln Asp Tyr Asp Thr Ser Val Pro Asn Trp Glu Phe Gly Lys Met Ile
333 225      230     235     240
335 Lys Glu Phe Arg Ala Thr Met Asp Cys His Arg Ile Ser Met Ala Asp
336      245     250     255
338 Pro Ala Glu Glu His Arg Ile Cys Val Cys Val Arg Lys Arg Pro Leu
339      260     265     270
341 Asn Lys Gln Glu Leu Ser Lys Lys Glu Ile Asp Ile Ile Ser Val Pro
342      275     280     285
344 Ser Lys Asn Ile Val Leu Val His Glu Pro Lys Leu Lys Val Asp Leu
345      290     295     300
347 Thr Lys Tyr Leu Glu Asn Gln Ala Phe Arg Phe Asp Phe Ser Phe Asp
348 305      310     315     320
350 Glu Thr Ala Thr Asn Glu Val Val Tyr Arg Phe Thr Ala Arg Pro Leu
351      325     330     335
353 Val Gln Ser Ile Phe Glu Gly Gly Lys Ala Thr Cys Phe Ala Tyr Gly
354      340     345     350
356 Gln Thr Gly Ser Gly Lys Thr His Thr Met Gly Gly Asp Phe Ser Gly
357      355     360     365
359 Lys Ser Gln Asn Val Ser Lys Gly Val Tyr Ala Phe Ala Ser Arg Asp
360      370     375     380
362 Val Phe Leu Leu Leu Asp Gln Pro Arg Tyr Lys His Leu Asp Leu Asp
363 385      390     395     400
365 Val Phe Val Thr Phe Glu Ile Tyr Asn Gly Lys Val Phe Asp Leu
366      405     410     415
368 Leu Asn Lys Lys Thr Lys Leu Arg Val Leu Glu Asp Ala Lys Gln Glu

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VERIFICATION SUMMARY

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Input Set : A:\04765-1.txt

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